

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 09/522,753 C
Source: IFW/b
Date Processed by STIC: 5/30/06

ENTERED



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/522,753C

DATE: 06/02/2006
TIME: 15:51:32

Input Set : A:\SALK1510.APP
Output Set: N:\CRF4\06022006\I522753C.raw

3 <110> APPLICANT: EVANS, RONALD M.
 4 CHEN, J. DON
 5 ORDENTLICH, PETER
 6 DOWNES, MICHAEL R.
 8 <120> TITLE OF INVENTION: FAMILY OF TRANSCRIPTIONAL CO-REPRESSORS THAT INTERACT
 9 WITH NUCLEAR HORMONE RECEPTORS AND USES THEREFOR
 11 <130> FILE REFERENCE: SALK1510-3
 13 <140> CURRENT APPLICATION NUMBER: 09/522,753C
 14 <141> CURRENT FILING DATE: 2000-03-10
 16 <150> PRIOR APPLICATION NUMBER: 08/522,726
 17 <151> PRIOR FILING DATE: 1995-09-01
 19 <160> NUMBER OF SEQ ID NOS: 52
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1495
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
 29 Met Glu Ala Trp Asp Ala His Pro Asp Lys Glu Ala Phe Ala Ala Glu
 30 1 5 10 15
 32 Ala Gln Lys Leu Pro Gly Asp Pro Pro Cys Trp Thr Ser Gly Leu Pro
 33 20 25 30
 35 Phe Pro Val Pro Pro Arg Glu Val Ile Lys Ala Ser Pro His Ala Pro
 36 35 40 45
 38 Asp Pro Ser Ala Phe Ser Tyr Ala Pro Pro Gly His Pro Leu Pro Leu
 39 50 55 60
 41 Gly Leu His Asp Thr Ala Arg Pro Val Leu Pro Arg Pro Pro Thr Ile
 42 65 70 75 80
 44 Ser Asn Pro Pro Pro Leu Ile Ser Ser Ala Lys His Pro Ser Val Leu
 45 85 90 95
 47 Glu Arg Gln Ile Gly Ala Ile Ser Gln Gly Met Ser Val Gln Leu His
 48 100 105 110
 50 Val Pro Tyr Ser Glu His Ala Lys Ala Pro Val Gly Pro Val Thr Met
 51 115 120 125
 53 Gly Leu Pro Leu Pro Met Asp Pro Lys Lys Leu Ala Pro Phe Ser Gly
 54 130 135 140
 56 Val Lys Gln Glu Gln Leu Ser Pro Arg Gly Gln Ala Gly Pro Pro Glu
 57 145 150 155 160
 59 Ser Leu Gly Val Pro Thr Ala Gln Glu Ala Ser Val Leu Arg Gly Thr
 60 165 170 175
 62 Ala Leu Gly Ser Val Pro Gly Gly Ser Ile Thr Lys Gly Ile Pro Ser
 63 180 185 190
 65 Thr Arg Val Pro Ser Asp Ser Ala Ile Thr Tyr Arg Gly Ser Ile Thr

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66	195	200	205
68	His Gly Thr Pro Ala Asp Val Leu Tyr Lys Gly Thr Ile Thr Arg Ile		
69	210	215	220
71	Ile Gly Glu Asp Ser Pro Ser Arg Leu Asp Arg Gly Arg Glu Asp Ser		
72	225	230	235
74	Leu Pro Lys Gly His Val Ile Tyr Glu Gly Lys Lys Gly His Val Leu		240
75	245	250	255
77	Ser Tyr Glu Gly Gly Met Ser Val Thr Gln Cys Ser Lys Glu Asp Gly		
78	260	265	270
80	Arg Ser Ser Ser Gly Pro Pro His Glu Thr Ala Ala Pro Lys Arg Thr		
81	275	280	285
83	Tyr Asp Met Met Glu Gly Arg Val Gly Arg Ala Ile Ser Ser Ala Ser		
84	290	295	300
86	Ile Glu Gly Leu Met Gly Arg Ala Ile Pro Pro Glu Arg His Ser Pro		
87	305	310	315
89	His His Leu Lys Glu Gln His His Ile Arg Gly Ser Ile Thr Gln Gly		320
90	325	330	335
92	Ile Pro Arg Ser Tyr Val Glu Ala Gln Glu Asp Tyr Leu Arg Arg Glu		
93	340	345	350
95	Ala Lys Leu Leu Lys Arg Glu Gly Thr Pro Pro Pro Pro Pro Pro Ser		
96	355	360	365
98	Arg Asp Leu Thr Glu Ala Tyr Lys Thr Gln Ala Leu Gly Pro Leu Lys		
99	370	375	380
101	Leu Lys Pro Ala His Glu Gly Leu Val Ala Thr Val Lys Glu Ala Gly		
102	385	390	395
104	400		
104	Arg Ser Ile His Glu Ile Pro Arg Glu Glu Leu Arg His Thr Pro Glu		
105	405	410	415
107	Leu Pro Leu Ala Pro Arg Pro Leu Lys Glu Gly Ser Ile Thr Gln Gly		
108	420	425	430
110	Thr Pro Leu Lys Tyr Asp Thr Gly Ala Ser Thr Thr Gly Ser Lys Lys		
111	435	440	445
113	His Asp Val Arg Ser Leu Ile Gly Ser Pro Gly Arg Thr Phe Pro Pro		
114	450	455	460
116	Val His Pro Leu Asp Val Met Ala Asp Ala Arg Ala Leu Glu Arg Ala		
117	465	470	475
119	480		
119	Cys Tyr Glu Glu Ser Leu Lys Ser Arg Pro Gly Thr Ala Ser Ser Ser		
120	485	490	495
122	Gly Gly Ser Ile Ala Arg Gly Ala Pro Val Ile Val Pro Glu Leu Gly		
123	500	505	510
125	515	520	525
128	Lys Pro Arg Gln Ser Pro Leu Thr Tyr Glu Asp His Gly Ala Pro Phe		
129	530	535	540
131	Ala Gly His Leu Pro Arg Gly Ser Pro Val Thr Met Arg Glu Pro Thr		
132	545	550	555
134	134 Arg Lys Leu Thr Ser Thr Pro Arg Glu Ile Ala Lys Ser Pro His Ser		560
135	565	570	575
137	137 Thr Val Pro Glu His His Pro His Pro Ile Ser Pro Tyr Glu His Leu		
138	580	585	590

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140 Leu Arg Gly Val Ser Gly Val Asp Leu Tyr Arg Ser His Ile Pro Leu
141      595          600          605
143 Ala Phe Asp Pro Thr Ser Ile Pro Arg Gly Ile Pro Leu Asp Ala Ala
144      610          615          620
146 Ala Ala Tyr Tyr Leu Pro Arg His Leu Ala Pro Asn Pro Thr Tyr Pro
147 625          630          635          640
149 His Leu Tyr Pro Pro Tyr Leu Ile Arg Gly Tyr Pro Asp Thr Ala Ala
150      645          650          655
152 Leu Glu Asn Arg Gln Thr Ile Ile Asn Asp Tyr Ile Thr Ser Gln Gln
153      660          665          670
155 Met His His Asn Thr Ala Thr Ala Met Ala Gln Arg Ala Asp Met Leu
156      675          680          685
158 Arg Gly Leu Ser Pro Arg Glu Ser Ser Leu Ala Leu Asn Tyr Ala Ala
159      690          695          700
161 Gly Pro Arg Gly Ile Ile Asp Leu Ser Gln Val Pro His Leu Pro Val
162 705          710          715          720
164 Leu Val Pro Pro Thr Pro Gly Thr Pro Ala Thr Ala Met Asp Arg Leu
165      725          730          735
167 Ala Tyr Leu Pro Thr Ala Pro Gln Pro Phe Ser Ser Arg His Ser Ser
168      740          745          750
170 Ser Pro Leu Ser Pro Gly Gly Pro Thr His Leu Thr Lys Pro Thr Thr
171      755          760          765
173 Thr Ser Ser Ser Glu Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg
174      770          775          780
176 Asp Arg Glu Arg Glu Lys Ser Ile Leu Thr Ser Thr Thr Thr Val Glu
177 785          790          795          800
179 His Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln Ser Ser Gly Ser Ser
180      805          810          815
182 Gly Ser Ser Gly Gly Gly Gly Ser Ser Ser Arg Pro Ala Ser His
183      820          825          830
185 Ser His Ala His Gln His Ser Pro Ile Ser Pro Arg Thr Gln Asp Ala
186      835          840          845
188 Leu Gln Gln Arg Pro Ser Val Leu His Asn Thr Gly Met Lys Gly Ile
189      850          855          860
191 Ile Thr Ala Val Glu Pro Ser Lys Pro Thr Val Leu Arg Ser Thr Ser
192 865          870          875          880
194 Thr Ser Ser Pro Val Arg Pro Ala Ala Thr Phe Pro Pro Ala Thr His
195      885          890          895
197 Cys Pro Leu Gly Gly Thr Leu Asp Gly Val Tyr Pro Thr Leu Met Glu
198      900          905          910
200 Pro Val Leu Leu Pro Lys Glu Ala Pro Arg Val Ala Arg Pro Glu Arg
201      915          920          925
203 Pro Arg Ala Asp Thr Gly His Ala Phe Leu Ala Lys Pro Pro Ala Arg
204      930          935          940
206 Ser Gly Leu Glu Pro Ala Ser Ser Pro Ser Lys Gly Ser Glu Pro Arg
207 945          950          955          960
209 Pro Leu Val Pro Pro Val Ser Gly His Ala Thr Ile Ala Arg Thr Pro
210      965          970          975
212 Ala Lys Asn Leu Ala Pro His His Ala Ser Pro Asp Pro Pro Ala Pro

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213	980	985	990
215	Pro Ala Ser Ala Ser Asp Pro His Arg Glu Lys Thr Gln Ser Lys Pro		
216	995	1000	1005
218	Phe Ser Ile Gln Glu Leu Glu Leu Arg Ser Leu Gly Tyr His Gly Ser		
219	1010	1015	1020
221	Ser Tyr Ser Pro Glu Gly Val Glu Pro Val Ser Pro Val Ser Ser Pro		
222	1025	1030	1035
224	1040	1045	1055
227	Ser Leu Thr His Asp Lys Gly Leu Pro Lys His Leu Glu Glu Leu Asp		
228	1055	1060	1065
230	Lys Ser His Leu Glu Gly Glu Leu Arg Pro Lys Gln Pro Gly Pro Val		
231	1070	1075	1080
233	Lys Leu Gly Gly Glu Ala Ala His Leu Pro His Leu Arg Pro Leu Pro		
234	1085	1090	1095
236	Glu Ser Gln Pro Ser Ser Pro Leu Leu Gln Thr Ala Pro Gly Val		
237	1100	1105	1110
239	Lys Gly His Gln Arg Val Val Thr Leu Ala Gln His Ile Ser Glu Val		
240	1115	1120	1125
242	Ile Thr Gln Asp Tyr Thr Arg His His Pro Gln Gln Leu Ser Ala Pro		
243	1130	1135	1140
245	Leu Pro Ala Pro Leu Tyr Ser Phe Pro Gly Ala Ser Cys Pro Val Leu		
246	1145	1150	1155
248	Asp Leu Arg Arg Pro Pro Ser Asp Leu Tyr Leu Pro Pro Pro Asp His		
249	1160	1165	1170
251	Gly Ala Pro Ala Arg Gly Ser Pro His Ser Glu Gly Gly Lys Arg Ser		
252	1175	1180	1185
254	Pro Glu Pro Asn Lys Thr Ser Val Leu Gly Gly Glu Asp Gly Ile		
255	1190	1195	1200
257	Glu Pro Val Ser Pro Pro Glu Gly Met Thr Glu Pro Gly His Ser Arg		
258	1210	1215	1220
260	Ile		
261	Ser Ala Val Tyr Pro Leu Leu Tyr Arg Asp Gly Glu Gln Thr Glu Pro		
263	1225	1230	1235
264	Ser Arg Met Gly Ser Lys Ser Pro Gly Asn Thr Ser Gln Pro Pro Ala		
266	1240	1245	1250
267	Phe Phe Ser Lys Leu Thr Glu Ser Asn Ser Ala Met Val Lys Ser Lys		
268	1255	1260	1265
269	Lys Gln Glu Ile Asn Lys Lys Leu Asn Thr His Asn Arg Asn Glu Pro		
270	1270	1275	1280
272	Glu Tyr Asn Ile Ser Gln Pro Gly Thr Glu Ile Phe Asn Met Pro Ala		
273	1285	1290	1295
275	Ile Thr Gly Thr Gly Leu Met Thr Tyr Arg Ser Gln Ala Val Gln Glu		
276	1300	1305	1310
278	His Ala Ser Thr Asn Met Gly Leu Glu Ala Ile Ile Arg Lys Ala Leu		
279	1315	1320	1325
281	Met Gly Lys Tyr Asp Gln Trp Glu Glu Ser Pro Pro Leu Ser Ala Asn		
282	1330	1335	1340
284	Ala Phe Asn Pro Leu Asn Ala Ser Ala Ser Leu Pro Ala Ala Met Pro		
285	1345	1350	1355
	1360	1370	1375

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Output Set: N:\CRF4\06022006\I522753C.raw

287 Gly Gly Gly Lys Ala Lys Val Ser Gly Arg Pro Ser Ser Arg Lys Ala
 288 1380 1385 1390
 290 Lys Ser Pro Ala Pro Gly Leu Ala Ser Gly Asp Arg Pro Pro Ser Val
 291 1395 1400 1405
 293 Ser Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr
 294 1410 1415 1420
 296 Asn Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe
 297 1425 1430 1435 1440
 299 Pro Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Val Met Ala Ser
 300 1445 1450 1455
 302 Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro
 303 1460 1465 1470
 305 His His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr
 306 1475 1480 1485
 308 Glu Thr Leu Ser Asp Ser Glu
 309 1490 1495
 312 <210> SEQ ID NO: 2
 313 <211> LENGTH: 46
 314 <212> TYPE: PRT
 315 <213> ORGANISM: Homo sapiens
 317 <400> SEQUENCE: 2
 318 His Ser Asp Val Ser Glu Ser Lys Arg Lys Arg Phe Glu Leu Asn Ser
 319 1 5 10 15
 321 Gly Glu Ala Gly Gly Asn Ala Thr Ser Ala Met Thr Asn Ser Ser Thr
 322 20 25 30
 324 Ser Gly Ser Met Asn Ile Ser Asn Ser His Gly Leu Lys Ala
 325 35 40 45
 328 <210> SEQ ID NO: 3
 329 <211> LENGTH: 17
 330 <212> TYPE: DNA
 331 <213> ORGANISM: Saccharomyces sp.
 333 <400> SEQUENCE: 3
 334 cggaggactg tcctccg 17
 337 <210> SEQ ID NO: 4
 338 <211> LENGTH: 8561
 339 <212> TYPE: DNA
 340 <213> ORGANISM: Homo sapiens
 342 <400> SEQUENCE: 4
 343 catgtcgggc tccacacagc ttgtggcaca gacgtggagg gccactgagc cccgctaccc 60
 344 gccccacagc ct当地ctacc cagtgcagat cggccggacg cacacggacg tc当地gctctt 120
 345 ggagtaccag caccactccc gc当地actatgc ct当地cacctg tc当地ggggct ccatcatcca 180
 346 gccccagcgg cggaggccct cc当地gtgtc tgagttccag cccggaaatg aacggtccca 240
 347 ggagctccac ct当地ggccag agtcccactc atacctgccg gagctggga agtcaagat 300
 348 ggagttcatt gaaagcaagc gc当地tcggct agagctgtc cctgacccccc tgctgcgacc 360
 349 gtcacccctg ct当地ccacgg gccagctgc gggatctgaa gacctcacca aggaccgtag 420
 350 cctgacgggc aagcttggAAC cggtgtctcc ccccaagcccc cc当地cacactg accctgagct 480
 351 ggagctgggt cccgcccccc tgtccaagga ggagctgatc cagaacatgg accgcgtgga 540
 352 cc当地agatc accatggtag agcagcagat ctcttaagctg aagaagaagc agcaacagct 600
 353 ggaggaggag gctgccaagc cggccgagcc tgagaagccc gtgtcaccgc cggccatcga 660

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/02/2006
PATENT APPLICATION: US/09/522,753C TIME: 15:51:33

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Output Set: N:\CRF4\06022006\I522753C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; N Pos. 109,8173,8180,8302,8343,8359,8384

Seq#:8; N Pos. 7250,7257,7379,7420,7436,7461

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L:1011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:60

M:341 Repeated in SeqNo=6

L:1780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:7200

M:341 Repeated in SeqNo=8